

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 3. (Canceled)

4. (Withdrawn) A computer-readable record medium in which a program that permits a computer to function as an identification system for cells, tissues or nuclei has been recorded, said identification system comprising:

(a) means for analyzing information on the methylation pattern of DNA isolated from a test cell, tissue or nucleus; and

(b) means for identifying the cell, tissue or nucleus using the analysis results as an indicator.

5. (Previously presented) A method of identifying the differentiation state of a test cell, tissue, or nucleus comprising:

obtaining a DNA methylation pattern for the test cell, tissue, or nucleus, wherein the DNA methylation pattern for the test cell, tissue, or nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state; and,

comparing the DNA methylation pattern for the test cell, tissue, or nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test cell, tissue, or nucleus is identified if the DNA methylation pattern of the test cell, tissue, or nucleus matches the differentiation state-specific DNA methylation pattern.

6. (Previously presented) The method of claim 5, wherein the DNA methylation pattern for the test cell, tissue, or nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Previously presented) The method of claim 17 or claim 18, further comprising determining nucleotide sequence information for differentially methylated gene regions that specify the differentiation state of the test cell, tissue, or nucleus.

8. The method of claim 5, wherein the test cell, tissue, or nucleus is a stem cell.

9. The method of claim 5, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 13. (Canceled)

14. (Withdrawn) A method of producing a differentiated cell, tissue, or nucleus comprising:

methylation or demethylation of the gene regions identified by the method of claim 7 in a cell, tissue, or nucleus, so as to specify a desired differentiation state; and

producing a differentiated cell, tissue, or nucleus.

15 - 16. (Canceled)

17. (Previously presented) The method of claim 5, wherein obtaining the differentiation state-specific DNA methylation pattern comprises:

obtaining a DNA methylation pattern for one or more cell, tissue, or nucleus of known differentiation state, wherein the DNA methylation pattern comprises information on the methylation state of CpG at a plurality of gene regions; and,

identifying gene regions that are differentially and specifically methylated for the cell, tissue, or nucleus of known differentiation state.

18. (Previously presented) The method of claim 17, wherein obtaining the differentiation state-specific DNA methylation pattern further comprises:

comparing the DNA methylation patterns for more than one cell, tissue, or nucleus of known differentiation state; and,

determining the methylation state of CpG at the differentially methylated gene regions for at least one of the more than one type of cell, tissue, or nucleus of known differentiation state, thereby obtaining a differentiation state-specific DNA methylation pattern.

19. (New) The method of claim 8, wherein the stem cell is an embryonic stem cell.

20. (New) The method of claim 5, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is differentiated.

21. (New) The method of claim 5, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is undifferentiated.

22. (New) A method of identifying a test cell, tissue, or nucleus, comprising:

obtaining a DNA methylation pattern for the test cell, tissue, or nucleus, wherein the DNA methylation pattern for the test cell, tissue, or nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of cell, tissue, or nucleus; wherein the one or more known types of cell, tissue, or nucleus is selected from undifferentiated embryonic stem cell, differentiated embryonic stem cell, undifferentiated trophoblast stem cell, differentiated trophoblast stem cell, kidney, placenta, brain, and sperm; and,

comparing the DNA methylation pattern for the test cell, tissue, or nucleus with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known cell, tissue, or nucleus;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated embryonic stem cell identifies the test cell, tissue, or nucleus as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated embryonic stem cell identifies the test cell, tissue, or nucleus as differentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test cell, tissue, or nucleus as undifferentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the differentiated trophoblast stem cell identifies the test cell, tissue, or nucleus as differentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the kidney identifies the test cell, tissue, or nucleus as kidney;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the placenta identifies the test cell, tissue, or nucleus as placenta;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the brain identifies the test cell, tissue, or nucleus as brain; and,

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the sperm identifies the test cell, tissue, or nucleus as sperm.

23. (New) The method of claim 22, wherein the DNA methylation patterns are obtained by generating RLGS profiles.